

Evaluation of frozen tissue-derived prognostic gene expression signatures in FFPE colorectal cancer samples

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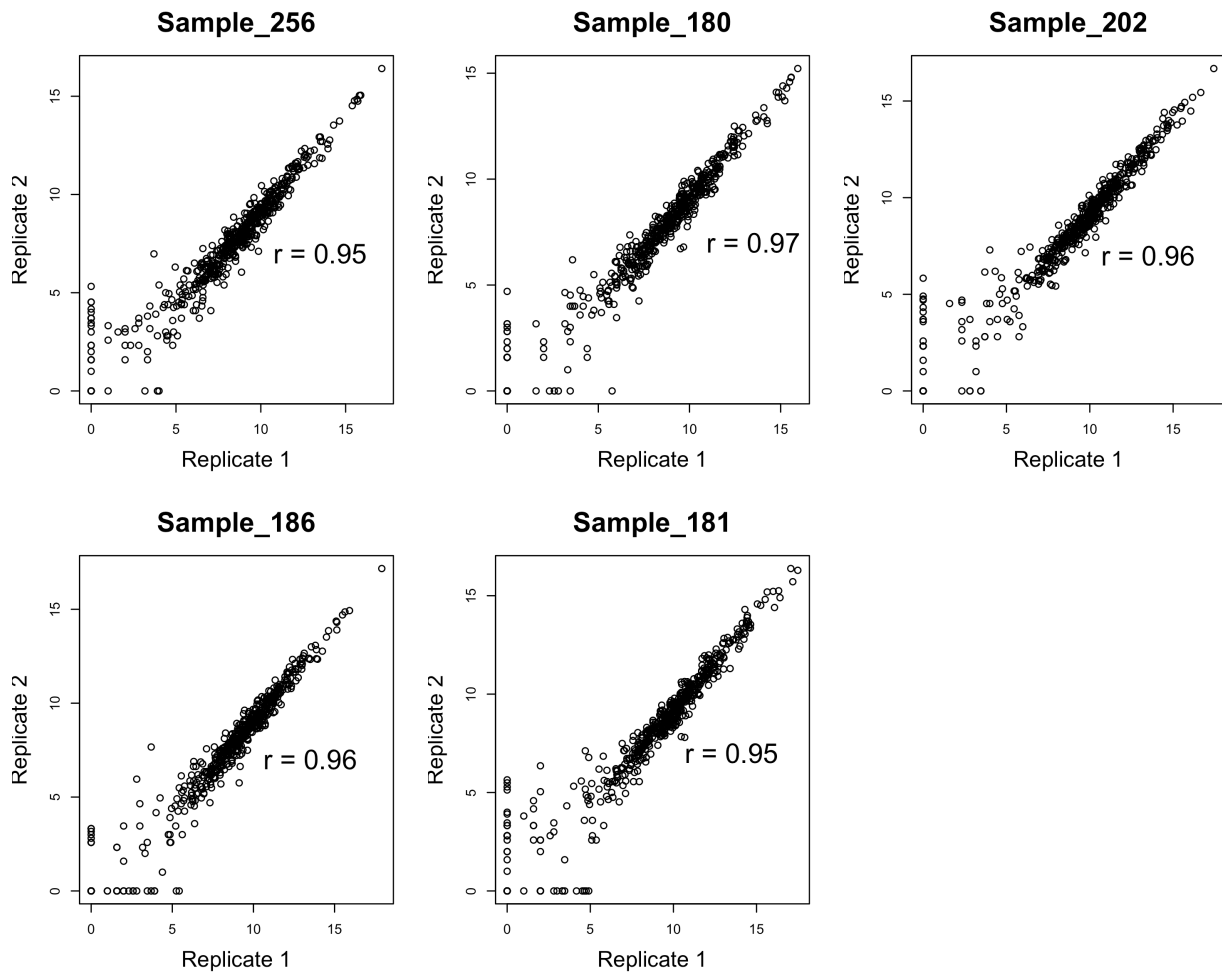
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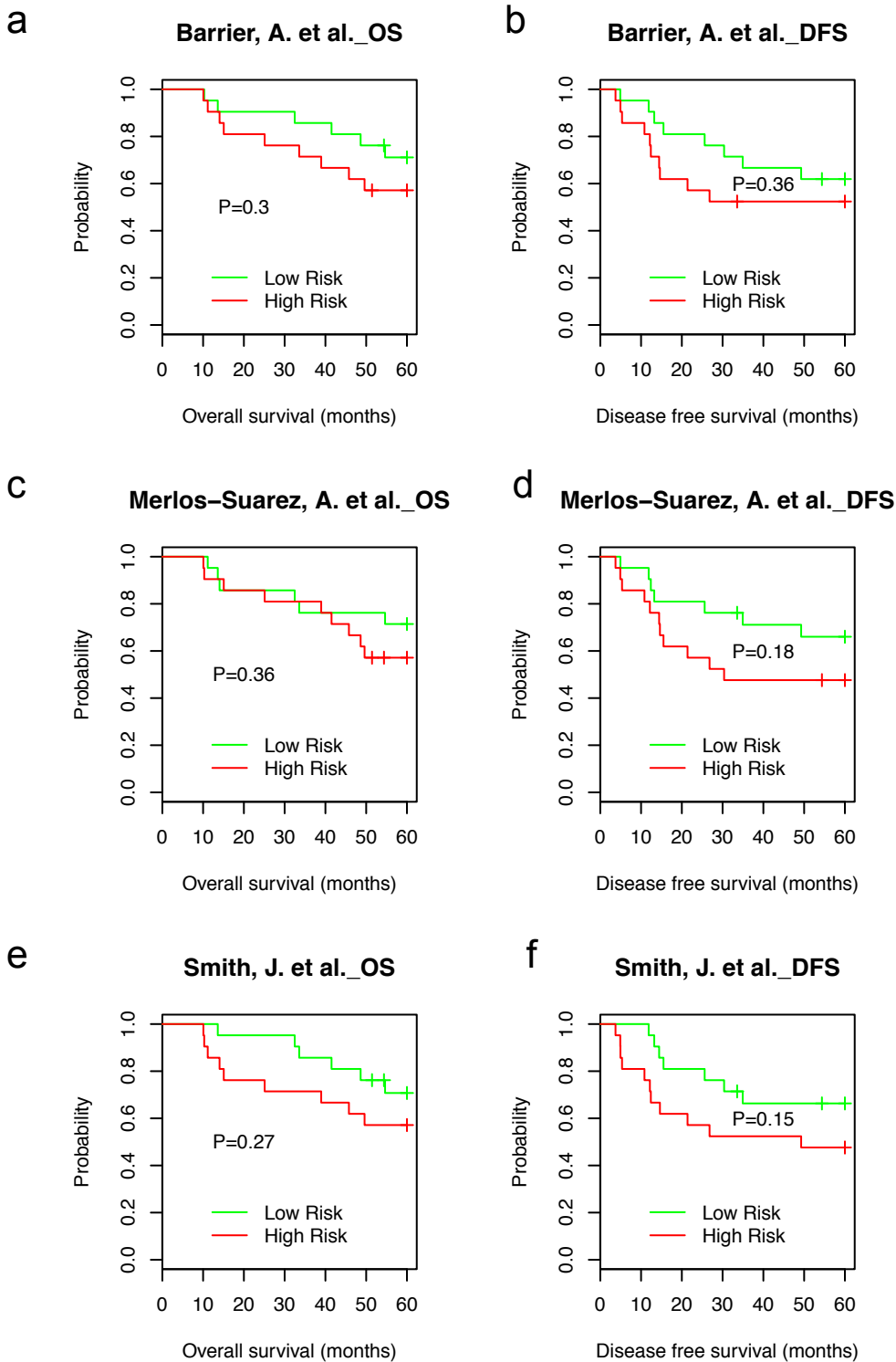
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Supplementary Figure S1. Scatterplot of the normalized counts from 536 individual gene elements using a split sample from single FFPE preserved tumor extraction on the nCounter platform. r shows the Pearson correlation coefficient.



Supplementary Figure S2. Performance of frozen-tissue derived prognostic signatures from Barrier, A. et al., Merlos-Suarez, A. et al. and Smith, J.J. et al. in FFPE-derived samples based on nCounter platform. Kaplan-Meier estimates of OS (a, c and e) and DFS (b, d and f) according to the risk prediction by gene signatures from Barrier, A. et al. (19 of 34 available genes), Merlos-Suarez, A. et al. (5 of 9 available genes) and Smith, J.J. et al. (13 of 31 available

genes) based on nCounter platform (42 samples were divided into two groups with 21 samples in each group).